

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: OPPER, Martin
BOSSLET, Klaus
CZECH, Joerg

(ii) TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
IN E. COLI

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Washington
(D) STATE: D.C.
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(F) ZIP: 20007-5109

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/630,820
(B) FILING DATE: 10-APR-1996

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE 19513676.4
(B) FILING DATE: 11-APR-1995

(viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Enterobacteriaceae: Escherichia coli

(vii) IMMEDIATE SOURCE:

(B) CLONE: KS + E.c.-Beta-Gluc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGCTTTCAT TGTTGCCTC CCTGCTGCGG

30

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Enterobacteriaceae: Escherichia coli

(vii) IMMEDIATE SOURCE:

(B) CLONE: KS + E.c.-Beta-Gluc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCTAGACCAT GGTACGTCCT GTACAAACCC CA

32

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pAB Stop c-DNA HC/hu-Beta-Gluc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAATTCCATG GAACCAGAAC CAGAACCGAG CTCAACTCT

39

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pAB Stop c-DNA HC/hu-Beta-Gluc

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCTAGATAAC GAGGGCAAAA AATGGAGGTC CAACTGCAGG AGAGC

45

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Enterobacteriaceae: Escherichia coli
 - (B) STRAIN: pRAJ210
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: pTrc99 dicistr. Fab/E.c.-Beta-Gluc
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..641
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 666..3162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CC ATG GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC
Met Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
1 5 10 15

47

GTG GGT GAC AGA GTG ACC ATC ACC TGT AGT ACC AGC TCG AGT GTA AGT
Val Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser Val Ser
20 25 30

95

TAC ATG CAC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG
Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

143

ATC TAC AGC ACA TCC AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC
Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

191

GGT AGC GGT AGC GGT ACC GAC TTC ACC ACC ATC AGC AGC CTC CAG Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln	65	70	75	239	
CCA GAG GAC ATC GCC ACC TAC TAC TGC CAT CAG TGG AGT AGT TAT CCC Pro Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro	80	85	90	95	287
ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGT ACT GTG GCT GCA Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala	100	105	110	335	
CCA TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG CAG TTG AAA TCT GGA Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly	115	120	125	383	
ACT GCC TCT GTT GTG TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG GCC Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala	130	135	140	431	
AAA GTA CAG TGG AAG GTG GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln	145	150	155	479	
GAG AGT GTC ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser	160	165	170	175	527
AGC ACC CTG ACG CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr	180	185	190	575	
GCC TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG CCC GTC ACA AAG AGC Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser	195	200	205	623	
TTC AAC AGG GGA GAG TGT TAGTCTAGAT AACGAGGGCA AAAA ATG GAG GTC Phe Asn Arg Gly Glu Cys	210		1	674	
CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA CCT AGC CAG ACC CTG Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu	5	10	15	722	
AGC CTG ACC TGC ACC GTG TCT GGC TTC ACC ATC AGC AGT GGT TAT AGC Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly Tyr Ser	20	25	30	35	770
TGG CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT GAG TGG ATT GGA Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly	40	45	50	818	
TAC ATA CAG TAC AGT GGT ATC ACT AAC TAC AAC CCC TCT CTC AAA AGT Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser	55	60	65	866	
AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC CAG TTC AGC CTG AGA Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg	70	75	80	914	
CTC AGC AGC GTG ACA GCC GAC ACC GCG GTC TAT TAT TGT GCA AGA Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg	85	90	95	962	
GAA GAC TAT GAT TAC CAC TGG TAC TTC GAT GTC TGG GGT CAA GGC AGC Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly Gln Gly Ser	100	105	110	115	1010

CTC GTC ACA GTC ACA GTC TCC TCA GCT TCC ACC AAG GGC CCA TCG GTC Leu Val Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val 120 125 130	1058
TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCT GGG GGC ACA GCG GCC Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala 135 140 145	1106
CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 150 155 160	1154
TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 165 170 175	1202
CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 180 185 190 195	1250
TCC AGC AGC TTG GGC ACC CAG ACC TAC ACC TGC AAC GTG AAT CAC AAG Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys 200 205 210	1298
CCC AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG CTC GGT TCT GGT TCT Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Gly Ser Gly Ser 215 220 225	1346
GGT TCC ATG GTA CGT CCT GTA GAA ACC CCA ACC CGT GAA ATC AAA AAA Gly Ser Met Val Arg Pro Val Glu Thr Pro Thr Arg Glu Ile Lys Lys 230 235 240	1394
CTC GAC GGC CTG TGG GCA TTC AGT CTG GAT CGC GAA AAC TGT GGA ATT Leu Asp Gly Leu Trp Ala Phe Ser Leu Asp Arg Glu Asn Cys Gly Ile 245 250 255	1442
GAT CAG CGT TGG TGG GAA AGC GCG TTA CAA GAA AGC CGG GCA ATT GCT Asp Gln Arg Trp Trp Glu Ser Ala Leu Gln Glu Ser Arg Ala Ile Ala 260 265 270 275	1490
GTG CCA GGC AGT TTT AAC GAT CAG TTC GCC GAT GCA GAT ATT CGT AAT Val Pro Gly Ser Phe Asn Asp Gln Phe Ala Asp Ala Asp Ile Arg Asn 280 285 290	1538
TAT GCG GGC AAC GTC TGG TAT CAG CGC GAA GTC TTT ATA CCG AAA GGT Tyr Ala Gly Asn Val Trp Tyr Gln Arg Glu Val Phe Ile Pro Lys Gly 295 300 305	1586
TGG GCA GGC CAG CGT ATC GTG CTG CGT TTC GAT GCG GTC ACT CAT TAC Trp Ala Gly Gln Arg Ile Val Leu Arg Phe Asp Ala Val Thr His Tyr 310 315 320	1634
GGC AAA GTG TGG GTC AAT AAT CAG GAA GTG ATG GAG CAT CAG GGC GGC Gly Lys Val Trp Val Asn Asn Gln Glu Val Met Glu His Gln Gly Gly 325 330 335	1682
TAT ACG CCA TTT GAA GCC GAT GTC ACG CCG TAT GTT ATT GCC GGG AAA Tyr Thr Pro Phe Glu Ala Asp Val Thr Pro Tyr Val Ile Ala Gly Lys 340 345 350 355	1730
AGT GTA CGT ATC ACC GTT TGT GTG AAC AAC GAA CTG AAC TGG CAG ACT Ser Val Arg Ile Thr Val Cys Val Asn Asn Glu Leu Asn Trp Gln Thr 360 365 370	1778
ATC CCG CCG GGA ATG GTG ATT ACC GAC GAA AAC GGC AAG AAA AAG CAG Ile Pro Pro Gly Met Val Ile Thr Asp Glu Asn Gly Lys Lys Lys Gln 375 380 385	1826

TCT TAC TTC CAT AAT TTC TTT AAC TAT GCC GGG ATC CAT CGC AGC GTA Ser Tyr Phe His Asn Phe Asn Tyr Ala Gly Ile His Arg Ser Val 390 395 400	1874
ATG CTC TAC ACC ACG CCG AAC ACC TGG GTG GAC GAT ATC ACC GTG GTG Met Leu Tyr Thr Thr Pro Asn Thr Trp Val Asp Asp Ile Thr Val Val 405 410 415	1922
ACG CAT GTC GCG CAA GAC TGT AAC CAC GCG TCT GTT GAC TGG CAG GTG Thr His Val Ala Gln Asp Cys Asn His Ala Ser Val Asp Trp Gln Val 420 425 430 435	1970
GTG GCC AAT GGT GAT GTC AGC GTT GAA CTG CGT GAT GCG GAT CAA CAG Val Ala Asn Gly Asp Val Ser Val Glu Leu Arg Asp Ala Asp Gln Gln 440 445 450	2018
GTG GTT GCA ACT GGA CAA GGC ACT AGC GGG ACT TTG CAA GTG GTG AAT Val Val Ala Thr Gly Gln Gly Thr Ser Gly Thr Leu Gln Val Val Asn 455 460 465	2066
CCG CAC CTC TGG CAA CCG GGT GAA GGT TAT CTC TAT GAA CTG TGC GTC Pro His Leu Trp Gln Pro Gly Glu Gly Tyr Leu Tyr Glu Leu Cys Val 470 475 480	2114
ACA GCC AAA AGC CAG ACA GAG TGT GAT ATC TAC CCG CTT CGC GTC GGC Thr Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr Pro Leu Arg Val Gly 485 490 495	2162
ATC CGG TCA GTG GCA GTG AAG GGC GAA CAG TTC CTG ATT AAC CAC AAA Ile Arg Ser Val Ala Val Lys Gly Glu Gln Phe Leu Ile Asn His Lys 500 505 510 515	2210
CCG TTC TAC TTT ACT GGC TTT GGT CGT CAT GAA GAT GCG GAC TTA CGT Pro Phe Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala Asp Leu Arg 520 525 530	2258
GGC AAA GGA TTC GAT AAC GTG CTG ATG GTG CAC GAC CAC GCA TTA ATG Gly Lys Gly Phe Asp Asn Val Leu Met Val His Asp His Ala Leu Met 535 540 545	2306
GAC TGG ATT GGG GCC AAC TCC TAC CGT ACC TCG CAT TAC CCT TAC GCT Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr Pro Tyr Ala 550 555 560	2354
GAA GAG ATG CTC GAC TGG GCA GAT GAA CAT GGC ATC GTG GTG ATT GAT Glu Glu Met Leu Asp Trp Ala Asp Glu His Gly Ile Val Val Ile Asp 565 570 575	2402
GAA ACT GCT GTC GGC TTT AAC CTC TCT TTA GGC ATT GGT TTC GAA Glu Thr Ala Ala Val Gly Phe Asn Leu Ser Leu Gly Ile Gly Phe Glu 580 585 590 595	2450
GCG GGC AAC AAG CCG AAA GAA CTG TAC AGC GAA GAG GCA GTC AAC GGG Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu Glu Ala Val Asn Gly 600 605 610	2498
GAA ACT CAG CAA GCG CAC TTA CAG GCG ATT AAA GAG CTG ATA GCG CGT Glu Thr Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu Ile Ala Arg 615 620 625	2546
GAC AAA AAC CAC CCA AGC GTG GTG ATG TGG AGT ATT GCC AAC GAA CCG Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala Asn Glu Pro 630 635 640	2594
GAT ACC CGT CCG CAA GGT GCA CGG GAA TAT TTC GCG CCA CTG GCG GAA Asp Thr Arg Pro Gln Gly Ala Arg Glu Tyr Phe Ala Pro Leu Ala Glu 645 650 655	2642

GCA ACG CGT AAA CTC GAC CCG ACG CGT CCG ATC ACC TGC GTC AAT GTA Ala Thr Arg Lys Leu Asp Pro Thr Arg Pro Ile Thr Cys Val Asn Val 660 665 670 675	2690
ATG TTC TGC GAC GCT CAC ACC GAT ACC ATC AGC GAT CTC TTT GAT GTG Met Phe Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu Phe Asp Val 680 685 690	2738
CTG TGC CTG AAC CGT TAT TAC GGA TGG TAT GTC CAA AGC GGC GAT TTG Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser Gly Asp Leu 695 700 705	2786
GAA ACG GCA GAG AAG GTA CTG GAA AAA GAA CTT CTG GCC TGG CAG GAG Glu Thr Ala Glu Lys Val Leu Glu Lys Glu Leu Ala Trp Gln Glu 710 715 720	2834
AAA CTG CAT CAG CCG ATT ATC ATC ACC GAA TAC GGC GTG GAT ACG TTA Lys Leu His Gln Pro Ile Ile Thr Glu Tyr Gly Val Asp Thr Leu 725 730 735	2882
GCC GGG CTG CAC TCA ATG TAC ACC GAC ATG TGG AGT GAA GAG TAT CAG Ala Gly Leu His Ser Met Tyr Thr Asp Met Trp Ser Glu Glu Tyr Gln 740 745 750 755	2930
TGT GCA TGG CTG GAT ATG TAT CAC CGC GTC TTT GAT CGC GTC AGC GCC Cys Ala Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg Val Ser Ala 760 765 770	2978
GTC GTC GGT GAA CAG GTA TGG AAT TTC GCC GAT TTT GCG ACC TCG CAA Val Val Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala Thr Ser Gln 775 780 785	3026
GGC ATA TTG CGC GTT GGC GGT AAC AAG AAA GGG ATC TTC ACT CGC GAC Gly Ile Leu Arg Val Gly Asn Lys Lys Gly Ile Phe Thr Arg Asp 790 795 800	3074
CGC AAA CCG AAG TCG GCG GCT TTT CTG CTG CAA AAA CGC TGG ACT GGC Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu Gln Lys Arg Trp Thr Gly 805 810 815	3122
ATG AAC TTC GGT GAA AAA CCG CAG CAG GGA GGC AAA CAA TGAAGCTT Met Asn Phe Gly Glu Lys Pro Gln Gln Gly Gly Lys Gln 820 825 830	3169

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val 1 5 10 15
Gly Asp Arg Val Thr Ile Thr Cys Ser Thr Ser Ser Ser Val Ser Tyr 20 25 30
Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile 35 40 45
Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Thr
85 90 95
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125
Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140
Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160
Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175
Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190
Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205
Asn Arg Gly Glu Cys
210

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 832 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser
1 5 10 15
Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser
20 25 30
Gly Tyr Ser Trp His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu
35 40 45
Trp Ile Gly Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser
50 55 60
Leu Lys Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80
Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp Gly
100 105 110
Gln Gly Ser Leu Val Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125
Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val
195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Leu Gly
210 215 220

Ser Gly Ser Gly Ser Met Val Arg Pro Val Glu Thr Pro Thr Arg Glu
225 230 235 240

Ile Lys Lys Leu Asp Gly Leu Trp Ala Phe Ser Leu Asp Arg Glu Asn
245 250 255

Cys Gly Ile Asp Gln Arg Trp Trp Glu Ser Ala Leu Gln Glu Ser Arg
260 265 270

Ala Ile Ala Val Pro Gly Ser Phe Asn Asp Gln Phe Ala Asp Ala Asp
275 280 285

Ile Arg Asn Tyr Ala Gly Asn Val Trp Tyr Gln Arg Glu Val Phe Ile
290 295 300

Pro Lys Gly Trp Ala Gly Gln Arg Ile Val Leu Arg Phe Asp Ala Val
305 310 315 320

Thr His Tyr Gly Lys Val Trp Val Asn Asn Gln Glu Val Met Glu His
325 330 335

Gln Gly Gly Tyr Thr Pro Phe Glu Ala Asp Val Thr Pro Tyr Val Ile
340 345 350

Ala Gly Lys Ser Val Arg Ile Thr Val Cys Val Asn Asn Glu Leu Asn
355 360 365

Trp Gln Thr Ile Pro Pro Gly Met Val Ile Thr Asp Glu Asn Gly Lys
370 375 380

Lys Lys Gln Ser Tyr Phe His Asn Phe Phe Asn Tyr Ala Gly Ile His
385 390 395 400

Arg Ser Val Met Leu Tyr Thr Thr Pro Asn Thr Trp Val Asp Asp Ile
405 410 415

Thr Val Val Thr His Val Ala Gln Asp Cys Asn His Ala Ser Val Asp
420 425 430

Trp Gln Val Val Ala Asn Gly Asp Val Ser Val Glu Leu Arg Asp Ala
435 440 445

Asp Gln Gln Val Val Ala Thr Gly Gln Gly Thr Ser Gly Thr Leu Gln
450 455 460

Val Val Asn Pro His Leu Trp Gln Pro Gly Glu Gly Tyr Leu Tyr Glu
465 470 475 480

Leu Cys Val Thr Ala Lys Ser Gln Thr Glu Cys Asp Ile Tyr Pro Leu
485 490 495

Arg Val Gly Ile Arg Ser Val Ala Val Lys Gly Glu Gln Phe Leu Ile
500 505 510

Asn His Lys Pro Phe Tyr Phe Thr Gly Phe Gly Arg His Glu Asp Ala
515 520 525

Asp Leu Arg Gly Lys Gly Phe Asp Asn Val Leu Met Val His Asp His
530 535 540

Ala Leu Met Asp Trp Ile Gly Ala Asn Ser Tyr Arg Thr Ser His Tyr
545 550 555 560

Pro Tyr Ala Glu Glu Met Leu Asp Trp Ala Asp Glu His Gly Ile Val
565 570 575

Val Ile Asp Glu Thr Ala Ala Val Gly Phe Asn Leu Ser Leu Gly Ile
580 585 590

Gly Phe Glu Ala Gly Asn Lys Pro Lys Glu Leu Tyr Ser Glu Glu Ala
595 600 605

Val Asn Gly Glu Thr Gln Gln Ala His Leu Gln Ala Ile Lys Glu Leu
610 615 620

Ile Ala Arg Asp Lys Asn His Pro Ser Val Val Met Trp Ser Ile Ala
625 630 635 640

Asn Glu Pro Asp Thr Arg Pro Gln Gly Ala Arg Glu Tyr Phe Ala Pro
645 650 655

Leu Ala Glu Ala Thr Arg Lys Leu Asp Pro Thr Arg Pro Ile Thr Cys
660 665 670

Val Asn Val Met Phe Cys Asp Ala His Thr Asp Thr Ile Ser Asp Leu
675 680 685

Phe Asp Val Leu Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Gln Ser
690 695 700

Gly Asp Leu Glu Thr Ala Glu Lys Val Leu Glu Lys Glu Leu Leu Ala
705 710 715 720

Trp Gln Glu Lys Leu His Gln Pro Ile Ile Ile Thr Glu Tyr Gly Val
725 730 735

Asp Thr Leu Ala Gly Leu His Ser Met Tyr Thr Asp Met Trp Ser Glu
740 745 750

Glu Tyr Gln Cys Ala Trp Leu Asp Met Tyr His Arg Val Phe Asp Arg
755 760 765

Val Ser Ala Val Val Gly Glu Gln Val Trp Asn Phe Ala Asp Phe Ala
770 775 780

Thr Ser Gln Gly Ile Leu Arg Val Gly Asn Lys Lys Gly Ile Phe
785 790 795 800

Thr Arg Asp Arg Lys Pro Lys Ser Ala Ala Phe Leu Leu Gln Lys Arg
805 810 815

Trp Thr Gly Met Asn Phe Gly Glu Lys Pro Gln Gln Gly Gly Lys Gln
820 825 830